



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: KEMBLE, George

Art Unit: 1648

Serial No. : 09/724,935

Examiner: Stacy B. Chen

Filed: November 28, 2000

Atty. Docket: CM101US

For: ATTENUATION OF CYTOMEGALOVIRUS VIRULENCE

PRELIMINARY AMENDMENT AND RESPONSE TO NOTICE TO COMPLY

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

In response to the Notice To Comply mailed February 14, 2005, and in accordance with 37 C.F.R.. §1.825(a)(b), please consider the following amendment and remarks. Applicants submit herewith: (a) a Preliminary Amendment entering a Substitute Sequence Listing; (b) a paper copy of the Substitute Sequence Listing (54 pages); (c) a computer readable form of said Substitute Sequence Listing (diskette); (d) a Statement Under 37 C.F.R. §1.825(a)(b); (e) a copy of the Notice To Comply; and (e) a Summary of an Examiner Interview and Comments therein.

Prior to examining the captioned application, Applicants respectfully request the entry of the following amendment and consideration of Applicants' comments.

Amendment begin on page 2 of this paper.

Summary and Comments begin on page 3 of this paper.

AMENDMENT

In the Sequence Listing:

Please delete the original sequence listing in its entirety and enter the attached Substitute Sequence Listing.

SUMMARY AND COMMENTS

The Substitute Sequence Listing contains sequences that were originally filed in Figures 1A to 1R, Figures 2A to 2H and as described in Table 2 (see page 41, line 29 to page 42, line 13) of the specification. Therefore, no new matter is introduced by the amendment.

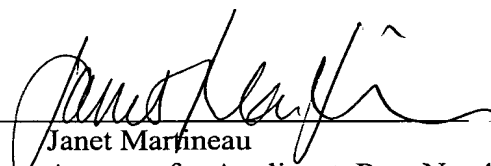
Applicants would like to thank the Examiner for taking the time to discuss the Notice to Comply With Sequence Rules. As discussed, Applicants have provided herewith a Substitute Sequence Listing including SEQ ID NOS only for the crossover regions in claims 13 and 14 (SEQ ID NOS: 28-31). The crossover points are disclosed in Table 2 of the specification (page 41, line 29 to page 42, line 13). Applicants wish to clarify that the crossover points refer to regions of homology with the HCMV reference strain, AD169, according to the nucleotide numbering convention of the AD169 genome (see specification at page 41 lines 18-25). The sequence of the AD169 genome was known well known in the art, publicly available from GenBank and the nucleotide numbering of the AD169 genome was commonly used as a reference for comparison of the genomic organization of HCMV strains.

As requested by the Examiner, below is a discussion of the methods used to characterize the HCMV chimeras. Briefly, a well characterized set of cosmids containing genomic regions from either the Towne and Toledo strains were used in the generation of each chimera (see specification at page 14, lines 15-30; Figure 5; page 36, lines 5-21; and Table 1). Thus, the choice of cosmids dictated to a large degree which genomic regions of the Towne and Toledo strains would be present. Confirmation of the genomic organization of the chimeras was performed by analysis of restriction enzyme pattern to confirm the identity of Towne-derived and Toledo-derived genomic regions. The limits of each Towne or Toledo-derived region were determined by sequence analysis of the ends of the cosmids used to generate the chimeras and their homology to the AD169 strain of HCMV using the nucleotide numbering convention of the AD169 genome (see specification at page 41, line 22-25 and Figure 10). Applicants also wish to direct the Examiner to page 40, line 4 to page 42, line 18 of the specification for addition details of the method used to generate and characterize the HCMV chimeras.

CONCLUSIONS

If the Examiner has any additional questions regarding the application or if the Examiner feels that an interview would expedite prosecution of this case, the Examiner is invited to call the undersigned.

Respectfully submitted,

By 
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Date: March 10, 2005

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